

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

**STAFF USE ONLY****Type of Search****Vendors and cost where applicable**

Searcher _____ <i>factb</i>	NA Sequence (#) _____	STN _____
Searcher Phone # _____	AA Sequence (#) _____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Other _____
Date Searcher Picked Up _____	Bibliographic _____	Dr Link _____
Date Completed <i>9-19-01</i>	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems _____
Cleical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____





us-09-285-480-175.rng

Sat Aug 26 19:26:24 2000

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2000, 20:27:28 ; Search time 64.49 Seconds  
(without alignments)  
4678.736 Million cell updates/sec

Title: US-09-285-480-175  
Perfect score: 1206  
Sequence: 1 ggcacgaggaagttttgtgt.....cgggtggtgtgtctgtgccc 1206

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149.4	12.4	367	V90219	EST clone DF670. N
2	69.4	5.8	116	T66409	DNA encoding haema
3	68.4	5.7	684	X33181	Base sequence of t
4	68.4	5.7	7372	X33182	Base sequence of t
5	68.4	5.7	7797	X33180	Cowpox virus bsr f
6	68.4	5.7	7996	X33184	Base sequence of t
7	63.8	5.3	9789	T41852	cDNA encoding Plas
8	59.4	4.9	3399	T05868	Chicken leucocytoz
9	56.4	4.7	110000	X20348_03	Continuation (4 of
10	54.6	4.5	1686	Q87387	DNA encoding Leuco
11	54.2	4.5	19124	T72882	Plasmodium var-7 g
12	53.8	4.5	5181	Q80911	Plasmodium falcipa
13	52.6	4.4	4237	V61487	Human secreted pro
14	52.6	4.4	116624	V52850	Human eval gene co
15	50.2	4.2	4663	X20373	Borrelia burgdorfe
16	49.8	4.1	110000	X20348_02	Continuation (3 of
17	48.2	4.0	2487	X20398	Borrelia burgdorfe
18	46.8	3.9	2892	X20392	Borrelia burgdorfe
19	45.2	3.7	4673	Q27189	P. yoellii SSP2 ant
20	44.8	3.7	1269	X20328	Borrelia burgdorfe
21	44.6	3.7	4590	N60472	Sequence encoding
22	44.6	3.7	110000	V21209_13	Continuation (14 o
23	44.4	3.7	4766	Q70102	Malarial PfEMP3 ep
24	44	3.6	1671	Q24134	50 KD subunit of S
25	44	3.6	9399	X20361	Borrelia burgdorfe
26	43.8	3.6	110000	V21209_02	Continuation (3 of
27	43.2	3.6	240	T76782	Staphylococcus aur
28	43.2	3.6	3095	Q03875	Sequence encoding
29	42.8	3.5	2447	V54387	Human secretory Pr
30	42.4	3.5	110000	X20348_08	Continuation (9 of
31	42	3.5	2973	Q53501	Sequence of bean m
32	42	3.5	35515	X20352	Borrelia burgdorfe
33	41.8	3.5	1956	T67161	Plasmodium falcipa

Human pro-urokinas  
B. burgdorferi Osp  
Streptococcus pneu  
Continuation (7 of  
Continuation (7 of  
NF-YB. Expression  
Mannose-1-phosphat  
P. falciparum gp19  
Sequence encoding  
Human secreted pro  
Nucleotide sequenc  
DNA encoding an an

34 41.6 3.4 2427 1 Q04107  
35 41.4 3.4 1498 1 Q83837  
36 41.2 3.4 1453 1 T61724  
37 40.8 3.4 110000 1 V21209\_06  
38 40.8 3.4 110000 1 X20248\_06  
39 40.6 3.4 1284 1 Q15361  
40 40.6 3.4 4000 1 T51902  
41 40.6 3.4 4940 1 V35363  
42 40.6 3.4 5760 1 N50530  
43 40.4 3.3 819 1 X04370  
44 40.2 3.3 202 1 V41451  
45 40.2 3.3 1434 1 X16007

## ALIGNMENTS

## RESULT 1

V90219

AC V90219: 19 standard; cDNA: 367 BP.

DT 15-FEB-1999 (first entry)

DE EST Clone DF670.

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

KW tissue growth; activin; inhibitor; chemotaxis; chemokinesis; haemostatic;

KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;

KW gene therapy; ss.

OS Homo sapiens.

PN W09845436-A2.

PD 15-OCT-1998: U06955.

PF 10-APR-1997: US-938821.

PA (GENY) GENETICS INST INC.

PI Agostino M, Jacobs K, Lavalie ER, McCoy JM, Merberg D.

PI Racie LA, Spaulding V, Treacy M;

DR WPI: 99-070077/06.

PT New polynucleotides encoding human secreted proteins - derived from

PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,

PT ovary, pituitary, retina and colon cDNA libraries.

PS Claim 1; Page 469; 618pp; English.

CC The present sequence represents a human expressed sequence tag (EST).

CC The polynucleotide, which is a secreted EST, and the encoded protein

CC are predicted to have useful biological activities which would make

CC them suitable for treating, preventing or ameliorating medical

CC conditions in humans and animals, although no supporting data is

CC given. Suggested activities include nutritional activity, immune

CC stimulating or suppressing activity, haematopoiesis regulating

CC activity, tissue growth activity, activin/inhibin activity,

CC chemotactic/chemokinetic activity, haemostatic and thrombolytic

CC activity, receptor/ligand activity, anti-inflammatory activity,

CC cadherin/tumour invasion suppressor activity, tumour inhibition

CC activity. The polynucleotide may also be useful for gene therapy.

CC Sequence 367 BP; 158 A; 53 C; 79 G; 77 T;

SQ

Query Match 12.4%; Score 149.4; DB 1; Length 367;

Best Local Similarity 67.5%; Pred. No. 4.1e-24;

Matches 241; Conservative 0; Mismatches 86; Indels 30; Gaps

QY 683 ttcagacatgcacaaagagacacacagctgaaacacagctgcaaatgaaggagctgaaca 742

DB 4 TTTAGCGGGGTACAAAGGACCTTAAGCCAAACACAGTGTCAATGAAGAAATGGAACA 63

QY 743 catgtatcaaaacgaacaaagataatgtgaaacacacactgaacagcagggagtctctaga 802

DB 64 AAAGTATCAAAATGACAAAGTAAAGTGATTAATATACATTTGGAAGCAGGAGTCTGTAGA 123

QY 803 tcagaaatttttcaactacaaagcaaaaaatgtggttccacagcgaattagttcattgc 862

DB 124 GGAGAGATTGTCCTCACTACAAAGTGAGATATGTTGCTTCGACAAACAATGGATGATGC 183

QY 863 acataagaagagctgacacacaaagcaagataacattgattacca----- 907

